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HUMAN-MURINE CHIMERIC ANTIBODIES AGAINST RESPIRATORY
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This invention relates to a human antibody which contains the one CDR from each variable heavy and variable light chain of at least one murine monoclonal antibody, against respiratory syncytial virus which is MAb1129 and the use thereof for the prevention and/or treatment of RSV infection. Data supplied from the esp@cenet database - Worldwide c7b

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(73) **MEDIMMUNE, INC.
35 West Watkins Mill
Road GAITHERSBURG XX (US).**

(72) **JOHNSON, Leslie Sid (US).**

(74) **SMART & BIGGAR**

(54) **ANTICORPS CHIMERIQUES HUMAINS-MURINS CONTRE LE VIRUS SYNCYTIAL RESPIRATOIRE**
(54) **HUMAN-MURINE CHIMERIC ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS**



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(72) JOHNSON, Leslie Sid, US

(73) MEDIMMUNE, INC., US

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(54) **ANTICORPS CHIMERIQUES HUMAINS-MURINS CONTRE LE
VIRUS SYNCYTIAL RESPIRATOIRE**

(54) **HUMAN-MURINE CHIMERIC ANTIBODIES AGAINST
RESPIRATORY SYNCYTIAL VIRUS**

(57) L'invention concerne un anticorps humain, qui contient la CDR (région déterminante de complémentarité) de chaque chaîne variable, lourde ou légère, d'un anticorps monoclonal murin au moins, MAbl129, qui s'oppose au virus respiratoire syncytial (RSV), et elle concerne son utilisation pour prévenir et/ou traiter une infection à RSV.

(57) This invention relates to a human antibody which contains the one CDR from each variable heavy and variable light chain of at least one murine monoclonal antibody, against respiratory syncytial virus which is MAbl129 and the use thereof for the prevention and/or treatment of RSV infection.





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(71) Applicant: MEDIMMUNE, INC. [US/US]; 35 West Watkins Mill Road, Gaithersburg, MD 20878 (US).			
(72) Inventor: JOHNSON, Leslie, Sld; 13545 Ambassador Drive, Germantown, MD 20874 (US).			
(74) Agents: FERRARO, Gregory, D. et al.; Carillo, Byrre, Bain, Guiliani, Cecchi, Stewart & Otencin, 6 Becker Farm Road, Rockville, NJ 07068 (US).			
(54) Title: HUMAN-MURINE CHIMERIC ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS			
(57) Abstract This invention relates to a human antibody which contains the one CDR from each variable heavy and variable light chain of at least one murine monoclonal antibody, against respiratory syncytial virus which is MAb1129 and the use thereof for the prevention and/or treatment of RSV infection.			

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Human-Murine Chimeric Antibodies Against
Respiratory Syncytial Virus

BACKGROUND

Respiratory syncytial virus (RSV) is the major cause
5 of acute respiratory illness in young children admitted to
hospitals, and the community practice will treat perhaps five
times the number of hospitalized children. It is therefore,
the most common cause of lower respiratory tract infection in
young children. While the majority of community-acquired RSV
10 infections resolve themselves in a week to ten days, many
hospitalized children, especially under six months of age
require assisted ventilation.

Efforts to produce an effective vaccine have been
unsuccessful (8). A major obstacle to vaccine development is
15 safety; the initial formalin inactivated RSV vaccine caused an
increased incidence of RSV lower respiratory tract disease and
death in immunized children upon exposure to virus (5).

Recently, the drug ribavirin has been licensed for
therapy of RSV pneumonia and bronchiolitis (2,3); its value is
20 controversial (4). Although ribavirin has shown efficacy (9),
the drug has to be administered over an 18 hour period

by aerosol inhalation. In addition, the level of secondary infections following cessation of treatment is significantly higher than in untreated patients.

Studies have shown that high-titered RSV immunoglobulin was effective both in prophylaxis and therapy for RSV infections in animal models (6, 7). Infected animals treated with RSV immune globulin, showed no evidence of pulmonary immune-complex disease (6, 7).

Even if RSV hyperimmune globulin is shown to reduce the incidence and severity of RSV lower respiratory tract infection in high risk children, several disadvantages may limit its use. One drawback is the necessity for intravenous infusion in these children who have limited venous access because of prior intensive therapy. A second disadvantage is the large volume of RSVIG required for protection, particularly since most these children have compromised cardiopulmonary function. A third disadvantage is that intravenous infusion necessitates monthly hospital visits during the RSV season which places these children at risk of nosocomial RSV infection (1). A final problem is that it may prove to be very difficult to select sufficient donors to produce a hyperimmune globulin for RSV to meet the demand for this product. Currently only about 8% of normal donors have RSV neutralizing antibody titers high enough to qualify for the production of hyperimmune globulin.

Another approach may be the development of monoclonal antibodies with high specific neutralizing activity as an alternative to hyperimmune globulin. It is preferable, if not necessary, to use human monoclonal antibodies rather than murine or rat antibodies to minimize the development of human anti-rodent antibody responses which may compromise the therapeutic efficacy of the antibody or induce immune-complex pathology. However, the generation of human monoclonal antibodies with the desired specificity may be difficult and

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the level of production from human cell lines is often low, precluding their development.

An alternative approach involves the production of human-mouse chimeric antibodies in which the genetic information encoding the murine heavy and light chain variable regions are fixed to genes encoding the heavy human and light constant regions. The resulting mouse-human hybrid has about 30% of the intact immunoglobulin derived from murine sequences. Therefore, although a number of laboratories have constructed chimeric antibodies with mouse variable and human constant domains (10-18), the mouse variable region may still be seen as foreign (19).

SUMMARY OF THE INVENTION

It is therefore an object of the present invention to provide a complementarity determining region (CDR) -grafted human antibody which contains at least one CDR from each variable heavy chain and variable light chain of at least one monoclonal antibody, against the RSV antigen. The monoclonal antibody may be derived from any non-human animal, preferably however, it is derived from a rodent and most preferably it is a murine monoclonal antibody. Preferably, the murine monoclonal antibody is a neutralizing antibody. It is also preferable that said murine antibody is an antibody against RSV F antigen.

In one embodiment, the invention provides a neutralizing antibody against respiratory syncytial virus (RSV), comprising: a human constant region and a variable region, said variable region comprising heavy and light chain framework regions and heavy and light chain complementarity determining regions (CDRs) at least a portion of the heavy and light chain framework regions being derived from a human antibody, said

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neutralizing antibody against RSV binding to the same epitope as an antibody comprising three heavy chain CDRs comprising amino acids 31-37, 52-67 and 100-109 of SEQ ID NO: 31, and three light-chain CDRs comprising amino acids 24-33, 51-56 and 89-96 of SEQ ID NO: 34.

In another embodiment, the invention provides a neutralizing antibody against respiratory syncytial virus, comprising: a human constant region and a heavy and light chain variable region said heavy and light chain variable region comprising heavy and light chain framework regions and heavy and light chain CDRs at least a portion of the heavy and light chain framework regions being derived from a human antibody, said CDRs comprising three heavy-chain CDRs comprising amino acids 31-37, 52-67 and 100-109 of SEQ ID NO: 31 and three light-chain CDRs comprising amino acids 24-33, 51-56 and 89-96 of SEQ ID NO: 34.

The term "animal" as used herein is used in its broadest sense includes mammals including humans.

DETAILED DESCRIPTION OF THE DRAWINGS

The drawings depicted and described herein are intended to further illustrate the present invention and are not intended to limit the invention in any manner whatsoever.

Figure 1 shows the amino acid (AA) sequence design of CDR-Grafted anti-RSV F glycoprotein V_H. The figure depicts

the AA sequence for the human HV3 V_H before grafting, CDR grafted V_H , and murine MAbl308F V_H from which the CDR sequence was grafted. The heavily underlined regions identify the CDR sequence which was grafted into the human HV3 V_H and each of the three regions is identified as CDR1, CDR2 and CDR3, respectively.

Figure 2 shows the amino acid (AA) sequence design of CDR-Grafted anti-RSV F Protein V_L . The figure depicts the AA sequence for the human K102 V_L before grafting, CDR grafted V_L , and murine MAbl308F V_L from which the CDR sequence was grafted. The heavily underlined regions identify the CDR sequence which was grafted into the human K102 V_L and each of the three regions is identified as CDR1, CDR2 and CDR3, respectively.

Figure 3 depicts the oligonucleotides used to make Hu1308F $_H$, the sequences which are underlined are the specific primer sequences.

Figure 4 depicts the oligonucleotides used to make Hu1308F $_L$, the sequences which are underlined are the specific primer sequences.

Figure 5 depicts the plasmid construction of the expression vectors for Humanized 1308.

Figure 6 depicts a graph of the Neutralization of RSV as percent neutralization versus ng MAb per reaction for neutralizing with Cos Hu1308F and with Mu1308F.

Figure 7 shows the amino acid (AA) sequence design of CDR-Grafted anti-RSV F glycoprotein V_H . The figure depicts the AA sequence for the human COR V_H before grafting, CDR grafted V_H , and murine MAbl129 V_H from which the CDR sequence was grafted. The heavily underlined regions identify the CDR sequence which was grafted into the human COR V_H and each of the three regions is identified as CDR1, CDR2 and CDR3, respectively.

Figure 8 shows the amino acid (AA) sequence design of CDR-Grafted anti-RSV F Protein V_L. The figure depicts the AA sequence for the human K102 V_L before grafting, CDR grafted V_L, and murine MAH129 V_L from which the CDR sequence was grafted. The heavily underlined regions identify the CDR sequence which was grafted into the human K102 V_L and each of the three regions is identified as CDR1, CDR2 and CDR3, respectively.

Figure 9 shows the oligonucleotides used to construct the humanized 1129 VH.

Figure 10 shows binding data for humanized 1129 in an ELISA assay.

DETAILED DESCRIPTION OF THE INVENTION

Applicants have found that transplantation into a human antibody, of only the genetic information for at least one CDR from each of the variable heavy and variable light chain derived from murine monoclonal antibody against RSV antigen, is effective for the prevention and treatment of RSV in animals. Preferably the murine antibody is a neutralizing antibody against RSV. Another aspect of the present invention provides for the murine antibody to be an antibody against RSV F antigen. Preferably, the murine antibody is neutralizing antibody against RSV F antigen. The substitution of the mouse CDR's into the human variable framework segments minimizes the potential for human anti-mouse antibody (HAMA) responses while retaining binding affinity and specificity for antigen, RSV F protein. Since, the CDR's do not contain characteristic murine or human motifs, the human antibodies containing the murine antibody CDR's are essentially indistinguishable from completely human antibodies, thereby, minimizing the human antibody response while retaining binding affinity and specificity for RSV F antigen.

The development of a humanized antibody against RSV F antigen began with a murine antibody against RSV F antigen. Examples of murine antibodies of this type are: Mab 1436C, Mab 113, Mab 112, Mab 151, Mab 1200, Mab 1214, Mab 1237, Mab 1129, Mab 1121, Mab 1107, Mab 131-1, Mab 43-1, Mab 1112, Mab 1269, Mab 1243, Mab 1331E, Mab 1308F and Mab 1302A (see citation 21).

An aspect of the present invention provides that the CDRs of the human antibody are comprised of three complementarity determining regions (CDRs) from each variable heavy and variable light chain of the murine antibody.

The murine antibodies against RSV F antigen have been mapped by competitive binding and reactivity profiles of virus escape mutants to three broad antigenic sites (A, B, C) containing 16 distinct epitopes (20). The epitopes within antigenic sites A and C have shown the least variability in natural isolates.

Therefore, another aspect of this invention provides for a human antibody containing at least one CDR from each variable heavy and variable light chain of at least one murine antibody against RSV F antigen which is specific for antigenic site A or C. In one aspect, this invention provides for the murine antibody against RSV F antigen specific for antigenic site C, where the murine antibody is Mab 1308F.

In such an embodiment of this invention a human antibody contains CDR's of the variable heavy chain of murine antibody Mab 1308F against the RSV F antigen. The CDR variable heavy chain of Mab 1308F comprises three CDRs having the following amino acid sequences: Nos. 31 to 35, 47 to 60 and 99 to 106. In addition, this embodiment contains CDR's of a variable light chain of Mab 1308F of murine antibody against RSV F antigen. The CDR variable light chain comprises three CDR's having the following amino acid sequences: Nos. 24 to 34, 50 to 56 and 89 to 97.

Another aspect of this invention provides for a human antibody containing at least one CDR from each variable heavy and variable light chain of at least one murine antibody against RSV F antigen which is specific for antigenic site C. Preferably, this invention provides for the murine antibody against RSV F antigen specific for antigenic site C, where the murine antibody is MAH 1129.

In the embodiment of this invention a human antibody which contains CDR's of the variable heavy chain of murine antibody MAH 1129 against the RSV F antigen. The CDR variable heavy chain of MAH 1129 comprises three CDRs having the following amino acid sequences: Nos. 31 to 36, 52 to 67 and 100 to 109. In addition, this embodiment contains CDR's of a variable light chain of MAH 1129 of murine antibody against RSV F antigen. The CDR variable light chain comprises three CDR's having the following amino acid sequences: Nos. 24 to 33, 51 to 56 and 89 to 96.

An additional aspect of applicants' invention is a process for preventing or treating RSV infection comprising administering to the animal an effective amount of a human antibody containing at least one CDR from each variable heavy and variable light chain, of at least one murine antibody against RSV F antigen.

Another aspect of applicants' invention is a composition comprising administering an effective amount of the human antibody as described above in conjunction with an acceptable pharmaceutical carrier. Acceptable pharmaceutical carriers include but are not limited to non-toxic buffers, fillers, isotonic solutions, etc.

The composition of Applicant's invention may be administered topically or systemically. Examples of topical administration are intranasal administration and inhalation of an aerosol containing the human antibody composition. Systemic administration may be accomplished by intravenous or intramuscular injection of the human antibody composition.

A preferred aspect of Applicants' invention is that the human antibody is administered as part of a plurality of human antibodies against RSV F antigen. These antibodies can be against the same or different epitopes of the RSV F antigen.

Additionally, the human antibody of this invention can be used clinically for diagnosing respiratory syncytial virus in patients. Because of their affinity for RSV F antigen these human antibodies can be used in known diagnostic assay procedures for detecting the presence and concentration of RSV F antigen cells in samples, e.g., body fluids. The human antibodies of the present invention can for example be attached or bound to a solid support, such as latex beads, a column, etc., which are then contacted with a sample believed to contain RSV F antigen.

Applicants' development of human antibodies against RSV, began with murine hybridoma cells producing murine monoclonal antibodies which have been shown to neutralize RSV *in vitro* and protect cotton rats against lower respiratory tract infection with RSV.

One such antibody was selected, which is specific for antigenic site C, to produce mouse-human chimeric antibodies. This antibody was chosen on the basis that it: (i) reacted with a large number of virus strains tested (at least 13 out of 14 isolated); (ii) retained neutralizing activity against virus escape mutants selected with other anti-F antibodies and (iii) blocked RSV replication when administered at low doses to cotton rats by intranasal route prior to virus challenge. The antibody showed significant reduction in pulmonary virus titer among antibodies in that respective region. Murine antibody 13087, specific for the C region of RSV F protein, was chosen as the initial target for humanization.

In summary, the human antibodies were constructed as follows: the RNA was extracted from the murine antibody-

producing cell line, the murine variable regions which are responsible for the binding of the antibody to RSV were cloned and sequenced, resulting in the identification of the murine antibody CDRs. Then a human variable heavy and light chain framework sequence having the highest homology with the variable heavy and light chain murine antibody, was selected. A human framework sequence such as described above is best able to accept the murine-derived CDRs.

The murine 1308F variable heavy chain was compared to various human germline genes, the highest homology was to the human germline gene HV3. The two sequences were 62% homologous overall and 65% in the framework regions. Significantly, there is good homology at the junctions of the CDR segments and the frameworks with the exception of the 5' end of FH2. The murine derived variable heavy chain CDRs were then substituted into the variable heavy chain human germline gene HV3. The mouse and human sequences as well as that of a potential CDR-Grafted combination of the two is shown in Figure 1.

A similar analysis of the V_L region revealed high homology to the human germ line V-Kappa gene K 102. The alignment of these sequences is shown in Figure 2. In this case the homology is 62% overall and 73% in the framework regions. The murine-derived variable light CDRs were then substituted into the human variable light chain of human germline gene K102. In each case a human J-region can be selected which is identical to the mouse sequence.

In another embodiment, murine 1129 variable heavy chain was compared to various human variable region amino acid sequences, the highest homology was to the human rearranged CDR sequence. The two amino acid sequences were 75% homologous overall and 80% in the framework regions. Significantly, there is good homology at the junctions of the CDR segments and the frameworks. The murine derived variable

heavy chain CDRs were then substituted into the variable heavy chain human CDR V_H sequence. The mouse and human sequences as well as that of a potential CDR-Grafted combination of the two is shown in Figure 1.

A similar analysis of the V_L region revealed high homology to the human germ line K102. The alignment of these sequences is shown in Figure 8. In this case the homology is 73% overall and 82% in the framework regions. The murine-derived variable light CDRs were then substituted into the human variable light chain of human germline K102. In this case a human J-region, human JK4, was selected which is similar to the mouse sequence.

Therefore, human antibodies are expressed and characterized relative to the parental murine antibodies to be certain that the genetic manipulation has not drastically altered the binding properties of the antibodies.

Applicants present herein examples which are further illustrative of the claimed invention but not intended to limit the invention.

Examples 1

cDNA cloning and sequencing of anti-BSV F Protein antibody 1308F

cDNA copies of the V_H and V_L of the target antibody were generated as follows. The first strand cDNA reaction was carried out using AMV reverse transcriptase and a phosphorylated oligonucleotide primer complementary to a segment of the mRNA coding for the constant region of the particular heavy or light chain isotype. For 1308F the isotype is gammal, kappa and the specific oligonucleotides were 5'AGCGATCCAGGGGCCAGTGGATAGAC complementary to codons 129-137 of the C μ region of the murine Gammal gene, and 5'TGATGGTGGGAAGATG complementary to codons 116-122 of the murine C-kappa gene. The primer anneals to a segment of the

mRNA adjacent to the variable region. Second strand cDNA synthesis was carried out using RNase H and *E. coli* DNA polymerase I, as described by Gubler and Hoffman (Gene 22, 463, 1983), followed by T4 DNA polymerase to assure that blunt ends are produced.

Signal	V	J	C	mRNA
	1st strand cDNA			
	2nd strand cDNA			

The ds-cDNA was ligated into pUC18 which had been digested with restriction endonuclease SmaI and treated with alkaline phosphatase. The ligation was used to transform *E. coli* DH5a by the method of Hanahan (J. Mol. Biol. 166:557, 1983). Oligonucleotide probes corresponding to C-region sequence lying between the first strand cDNA primer and the V-region were used in colony hybridizations to identify transformants carrying the desired cDNA segment. The specific probe sequences were GGCCAGTGGATAGAC complementary to codons 121-125 of murine CH1 regions and TACAGTTGGTGCAGCA complementary to codons 110-115 of c-Kappa, respectively. Candidate plasmids, isolated from colonies which were positive in the hybridization, were analyzed by digestion with restriction endonucleases Eco RI and Hind III to release the cDNA insert. Those with inserts of 400-500bp were subjected to DNA sequencing.

The cDNA inserts were inserted into M13 mp18 and mp19 for the determination of the DNA sequence on both strands. Single stranded DNA from the resulting recombinant bacteriophage was isolated and sequenced by the dideoxy chain termination method (Proc. Nat. Acad. Sci. USA 74: 5463, 1977).

In order to confirm that the pair of rearranged and somatically mutated V gene cDNA's isolated from the 1308F hybridoma represented those which were in the 1308F antibody, a single-chain Fv gene was generated, expressed in and secreted from mammalian cells, then assayed for binding to RS virus. Competition binding experiments then were used to demonstrate the identity of the binding site.

Example 2

Design and assembly of human 1308F V_H and V_L

The CDR regions of the V_H and V_L were identified by comparing the amino acid sequence to known sequences as described by Kabat (38). In order to select the human framework sequences best able to accept the mouse derived CDR sequences in a conformation which retains the structure of the antigen combining site, the following strategy was employed. First, the sequence of the murine V_H and V_L regions will be compared to known human sequences from both the Genbank and NBRF protein databanks using the Wordsearch program in the Wisconsin package of sequence manipulation programs (Nucleic Acid Res. 12:387). The best several human V-regions were then analyzed further on the basis of similarity in the framework regions, especially at the junctions of the framework and CDR regions (see Figures 1 and 2).

The CDR-grafted V_H region together with the respective leader sequence of the human v-region gene was synthesized de novo using four overlapping oligonucleotides ranging from 100-137 nucleotides in length (see Figure 3). The oligonucleotides were first allowed to anneal in pairwise combinations and extended with DNA polymerase to generate approximately 200bp ds DNA fragments with an overlapping region. the fragments were then mixed and subjected to PCR using primers at the 3' end of one fragment and the 5' end of

the other fragment. The only product which can be formed under these conditions is the full length V_H segment. The specific primer sequences are underlined in Figure 3. An endonuclease Sac I site was included at the 3' end of the V_H sequence in order to join it to a human constant region gene segment.

The CDR-grafted V_L region was synthesized in a similar way (see Figure 4). In this instance the initial 206bp fragments were amplified separately and inserted into separate plasmids. The fragment coding for the amino terminus was cloned into a pUC18 derivative as an NcoI-SmaI fragment while the fragment coding for the carboxyl-terminus was cloned as a SmaI to Hind III fragment. The fragments were subsequently combined via a SmaI site at the junction. The oligonucleotides are indicated in Figure 4. A Hind III site was included near the 3' end of the gene segment in order to join it to a human C-kappa gene.

Example 1

Construction of Vectors for 1308F expression

The NcoI-SacI fragment representing the humanized V_H was joined to a SacI-NotI fragment representing a human c-Gamma I CDNA and inserted into pS 18 (which is pUC 18 with NcoI and NotI restriction sites incorporated into the polylinker region between the BamHI and KpnI sites). The humanized 1308F-gamma1 gene on a SacI-NotI fragment was then combined with a PvuI-NotI fragment from pSJ37 carrying a poly A addition site and a PvuI-SacI fragment from pSV2-dhfr-pCMV containing the SV40 origin of replication, a dhfr gene and the CMV immediate early promoter. The resulting plasmid was designated pSJ60.

The NcoI-HindIII fragment representing the humanized V_L was joined to a HindIII-NotI fragment representing a human c-

Kappa CNA in pS18. The humanized 1308F-Kappa gene on a SalI-NotI fragment was then combined with a PvuI-NotI fragment from pSJ37 carrying a poly A addition site and a PvuI-SalI fragment from pSV2-dhfr-pCMV, containing the SV40 origin of replication, a dhfr gene and the CMV immediate early promoter. The resulting plasmid was designated pSJ61.

Finally pSJ60 and pSJ61 were combined into a single plasmid containing both the light and heavy chains and expression signals. This was accomplished by isolating a PvuI-Bam HI fragment from pSJ61 carrying the light chain with a Pvu I - Bgl II fragment from pSJ60 carrying the heavy chain to generate pSJ66. (See Figure 5).

Example 4

Transfection of COS1 cells with pSJ60 and pSJ61

Transfections were carried out according to the method of McCutchan and Pagano (J. Nat. Can. Inst. 41: 351-356, 1968) with the following modifications. COS 1 cells (ATCC CRL1650) were maintained in a humidified 5% CO2 incubator in 75 cm² tissue culture flasks in Dulbecco's Modified Eagle Medium (DMEM, GIBCO #320-1965) supplemented with 10% Fetal Bovine Serum (FBS, GIBCO #200-6140) and 2mM L-glutamine (BRL #320-5030) and passed at a split ratio of 1:20 when the cells had reached confluence. 48 hours prior to transfection, 5 100mm tissue culture dishes were seeded with 1.5×10^6 cells per dish in 12ml DMEM, 10% FBS, 2mM L-glutamine, 1% penicillin-streptomycin (P-S, GIBCO #600-5070). The day of the transfection, 120 ug each of the plasmids pSJ60 and pSJ61 were combined, ethanol precipitated, and aseptically resuspended in 2.5ml Tris-Buffered-Saline. The resuspended DNA was added dropwise, with mixing, to 10ml of DMEM containing 1 mg/ml DEAE-dextran (Pharmacia #17-0350-01) and 250 uM chloroquine (Sigma #C5628). The medium was removed from the COS1 cells in the 100 mm dishes and the cells were

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- Washed once with Dulbecco's phosphate buffered saline (D-PBS, GIBCO #310-4190), and 2.5ml DMEM supplemented with 10% NuSerum* (Collaborative Research #55000) were added to each plate. 2.5ml of the DNA/DEAE-dextran/chloroquine mix were
- 5 added dropwise to each plate, the plates swirled to mix the DNA, and were returned to the incubator. After 4 hours in the incubator, the supernatant was aspirated from the cells and the cells were washed once with 5ml D-PBS. The cells were shocked for 3 minutes by the addition of 5ml of 10% dimethylsulfoxide
- 10 (DMSO) in D-PBS at room temperature. The DMSO was aspirated from the cells and the cells were washed with 5ml D-PBS. 14ml of DMEM/10% FBS/2mM L-glutamine/1%P-S were added to each plate and the plates were returned to the incubator.

- Three days post-transfection the medium was removed
- 15 from the plates, pooled, and stored at -20°C. The cells were harvested, pooled, and seeded into 4 150cm² tissue culture flasks two with 40ml DMEM/10% NuSerum and two with 40ml DMEM/10% FBS/2mM L-glutamine. The medium was collected and the cells refed at 7, 10, and 14 days. In this way a total of
- 20 125ug of humanized 1308F antibody was accumulated in 310ml of medium supplemented with FBS and 85ug in 240ml of medium supplemented with NuSerum.

Example 5

Transfections of COS 1 cells with PSJ66

- 25 48 hours prior to transfection, 5 100mm tissue culture dishes were seeded with 1.5×10^6 cells per dish in 12ml DMEM, 10% FBS, 2mM L-glutamine, 1% penicillin-streptomycin (P-S, GIBCO #600-5070). The day of the transfection, 125ug of

*Trade-mark

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the plasmid pSJ66 were ethanol precipitated and aseptically resuspended in 1.0 ml Tris-Buffered-Saline. The resuspended DNA was added dropwise, with mixing, to 4.0ml of DMEM containing 1mg/ml DEAE-dextran (pharmacia #17-0350-01) and

250µM chloroquine (Sigma #C5626). The medium was removed from the COS1 cells in the 100mm dishes and the cells were washed once with Dulbecco's phosphate buffered saline (D-PBS, GIBCO #310-4190), and 2.5ml DMEM supplemented with 10% NuSerum (Collaborative Research #55000) were added to each plate. 2.5ml of the DNA/DEAE-dextran/chloroquine mix were added dropwise to each plate, the plates swirled to mix the DNA, and were returned to the incubator. After 4 hours in the incubator, the supernatant was aspirated from the cells and the cells were washed once with 5ml D-PBS. The cells were shocked for 3 minutes by the addition of 5ml of 10% dimethylsulfoxide (DMSO) in D-PBS at room temperature. The DMSO was aspirated from the cells and the cells were washed with 5ml D-PBS. 14ml of DMEM/10% FBS/2mM L-glutamine/14P-S were added to each plate and the plates were returned to the incubator.

Three days post-transfection the medium was removed from the plates, pooled, and stored at -20°C. The cells were harvested, pooled, and seeded into 4 150cm² tissue culture flasks two with 40 ml DMEM/10% NuSerum and two with 40 ml DMEM/10% FBS/2mM L-glutamine. The medium was collected and the cells refed at 7, 10, and 14 days. In this way a total of 190µg of humanized 1308F antibody was accumulated in 310ml of medium supplemented with FBS and 120µg in 240ml of medium supplemented with NuSerum.

The concentration of humanized 1308F antibody secreted from the Cos1 cells into the medium was determined using a capture ELISA. Goat anti-human IgG Fc coated onto 96 well plates was used to capture the humanized antibody. Peroxidase conjugated goat anti-human whole IgG developed with a chromogenic substrate was then used to detect the bound antibody. A purified human IgG1/Kappa preparation was used to calibrate the assay.

Example 6Neutralization of RSV with humanized 1308FMETHODS:

RSV was neutralized with either humanized 1308F from Cos cell supernatant or purified 1308F murine monoclonal antibody. This was done by incubating 50 plaque-forming units of RSV with serial 2-fold dilutions of antibody for 1.0 hour at 37°C. Confluent monolayers of Hep2 cells in 24 well panels were infected with 100µl of antibody treated virus, untreated control virus, and mock infected controls. Incubated for 1.5 hours at 37°C, humidified, and 5% CO₂ and overlaid with 1.5mL EMEM, 1% FBS, and 1% methyl cellulose. Cells were fixed and stained with glutaraldehyde and crystal violet on day 4. Plaques were counted in triplicate wells and plotted as percent neutralization. The results shown in Figure 6 indicate that both the purified murine 1308F monoclonal and the humanized 1308F monoclonal antibody at 5 to 10 ng per well yield similar 50% reductions in RSV plaques.

Example 7Generation of a CDR-grafted λ-site antibody 1129

Poly-A⁺ RNA was purified from a lysate of 2 x 10⁷ murine 1129 hybridoma cells using oligo-dt cellulose. First strand cDNA was made from 1 µg pA⁺ RNA using random hexamer primers and AMV reverse transcriptase* 1µg pA⁺ RNA, 50mM Tris-HCl pH 8.5, 8mM MgCl₂, 30mM KCl, 1 mM dithiothreitol, 1 mM dNTP's, 25 units of placental ribonuclease inhibitor, 33µM random hexamer and 10 units of AMV reverse transcriptase for one hour at 42°C. The cDNA from the 1129 VL region was amplified by PCR using oligonucleotides SJ41 and SJ11, see Table 1. cDNA from the 1129 VH region was similarly amplified using oligonucleotides SJ42 and SJ10, see Table 1.

TABLE 1

SJ10
ACCGGATCCAGGGGCCAGTGGATAGAC

SJ11
GATGGATCCAGTTGGTGCGAGCATC

SJ41
CACGTGACATTGAGCTGACCCAGTCTCCA

SJ42
CGGAATTGAGGTTTAACTGCAGTAGTC(A,T)GG
{T = deoxy-Inosine}

SJ53
CCCAAGCTTGGTCCCCCCTCCGAACGTG

SJ154
GGCGTCGACTCACCATGGACATGAGGTTCC(C/T)CGCTCAGC

SJ155 (H1129L CDR 1)
GTCAACATCACTGCAAGTGCAGCTGAGTGTAGGTTACATGCACTGGTACC
AGCAG

SJ157 (H1129L CDR 3)
GGCACTTATTACTGCTTTCAGGGGAGTGGGTACCCATTCACTTCGAGAGGG
GG

SJ168
GTGACCAACATGGAACCTGCTGATACCTGCCAC

SJ169
CCATGTTGGTCACTTTAAGGAACCACTGG

SJ170

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CCAGTTTACTAGTGTTCATAGATCAGGAGCTTAGGGGC

SJ171

TGACACTAGTAAACTGGCTTCTGGGGTCCCATCAAG

5

PCR conditions

0.5uL of 1st strand cDNA, 10mM Tris-HCl pH 8.3, 50mM KCl, 1.5mM Mg₂Cl, 0.2mM dNTP's, 0.001 % gelatin, 1uM each primer, 1ng DNA template and 2.5u AmpliTaq(TM) DNA polymerase(Perkin Elmer -

10 Cetus). 94° 1 minute, 55° 2 minutes, 72° 2 minutes in Perkin Elmer 480 thermocycler for 25 cycles. The resulting DNA fragment (s) were then extracted once with phenol/chloroform (1/1), precipitated with 2.5 volumes of ETOH, resuspended in the appropriate restriction endonuclease buffer and digested

15 with restriction endonucleases to produce cohesive ends for cloning. The resulting fragments were then separated by electrophoresis on a 1 % agarose gel. After staining the gel with ethidium bromide the fragments were excised and purified from the agarose by freezing and extraction in the presence of

20 phenol.

The fragments were then digested with restriction endonucleases EcoR1 and BamH1 and cloned into plasmid pUC18. The inserts were then sequenced by the dideoxynucleotide chain termination method using modified T7 DNA polymerase (Sequeunase*, US

25 Biochemical).

The translated sequences were compared to human antibody

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protein sequences. The VL was found to be most homologous to the K102 light chain and the VH was found to be most homologous to the Cor VH region. The 1129 Fv region was then modeled by substitution of the residues from the 1129 VL and VH sequence
5 into the coordinates of corresponding residues in the crystal structure the MCPC603 antibody. Residues were

identified as being integral to the folded structure or solvent exposed by visual inspection of the model.

Several residues which were integral and which were different in the mouse and human sequences were left as the mouse residue in order to maintain the integrity of the Fv and thus the binding site. Such residues were 31,83,113, and 116 on the VH and 47 in the VL region. The resulting sequences are shown in figures 7 and 8.

The designed humanized 1129 VH was constructed using synthetic oligonucleotides SJ147-SJ153 (Figure 9) which were combined using PCR. The products of this PCR were then digested with NcoI and SacI and cloned into plasmid vector pSJ40 which is a pUC18 derivative in which an out of frame lacZ1 segment is restored in frame as a fusion to an in-frame V region segment when such a segment is inserted as an NcoI-SacI fragment. A plasmid containing an insert in which 5 mutations were clustered in a single 50 bp region was then subjected to repair of these changes using recombinant PCR and the primers SJ168 and SJ169, see Table 1.

The VL was generated by site directed mutagenesis of the humanized 1308F light chain gene. Oligonucleotides SJ155, see Table 1, (CDR1), and SJ157 (CDR3) were used to separately mutagenize the H1308L gene. Mutagenesis was carried out using T7 DNA polymerase on uracil containing single stranded DNA templates generated in *E. coli* strain BW313 (dut-, ung-) and subsequently transformed into *E. coli* strain DH5 (dut+, ung+). The two mutants were combined and CDR2 introduced by recombinant PCR using oligonucleotides SJ170, SJ154, see Table 1, (5'end) and SJ171, SJ53, see Table 1, (3'end). The CDR-grafted VH and VL genes were placed into pSJ60 (see Example 3) and pSJ61 (see Example 3), respectively as NcoI-SacI fragments in place of the H1308F V region

segments resulting in plasmids pSJ81 and pSJ105. In addition the murine VH and VL cDNA segments were similarly joined to human C-Gamma1 and Ckappa respectively to generate expression vectors pSJ75 and pSJ84.

Example 8

Hu1129 Transient Expression

COS1 cells (ATCC CRL1650) were maintained in a humidified 5% CO₂ incubator in 75 CM² tissue culture flasks in Dulbecco's Modified Eagle Medium (DMEM, GIBCO #320-1965) supplemented with 10% fetal bovine serum (FBS, GIBCO #200-6140) and 2mM L-glutamine (GIBCO #320-5030) and passed at a split ratio of 1:20 just prior to reaching confluence.

Transfections were carried out according to the method of McCutchan and Pagano (J. Nat. Can. Inst. 41: 351-356, 1968) with the following modifications. Twenty four hours prior to transfection 100 mm tissue culture dishes (Corning # 25020) were seeded with 2 x 10⁶ COS1 cells per dish in 14 ml DMEM, 10% FBS, 2mM L-glutamine. The day of the transfection 10 ug of the Hu1129 heavy chain plasmid (pSJ81, from Example 7) were combined with 10 ug of the Hu1129 kappa light chain plasmid pSJ105, from Example 7, the DNA was ethanol precipitated and aseptically resuspended in 1.0 ml Tris-Buffered-Saline. The resuspended DNA was added dropwise, with mixing, to 4.0 ml of DMEM containing 1 mg/ml DEAE-dextran (Pharmacia #170350-01) and 250 uM Chloroquine (Sigma #C6628). The medium was removed from the COS1 cell dishes, the cell monolayers were washed once with 10 ml Dulbecco's phosphate buffered saline (D-PBS, GIBCO #310-4190), and 2.5 ml DMEM supplemented with 10% NuSerum (Collaborative Research #55000) and 2mM L-glutamine were added to each plate. 2.5 ml of the DNA/DEAE-dextran/chloroquine mix were added dropwise to each plate.

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the plates were swirled to mix the DNA, and returned to the incubator. After an eight hour DNA adsorption period the plates were removed from the incubator and the supernatant was aspirated from the plates. The cells were shocked by the
 5 addition of 5 ml of 10% DMSO in D-PBS per plate for 3 minutes at room temperature, after which the DMSO was aspirated from the cells and the cells were washed once with 5 ml D-PBS. 15 ml DMEM, 10% NuSerum, 2mM L-glutamine (production medium) were added to each plate and the plates were returned to the
 10 incubator.

Seventy two hours post-transfection the conditioned medium was harvested from the plates and stored at -20°C, and 5 ml production medium was added to the plates and the plates were returned to the incubator. Ninety six hours later the
 15 medium was collected from the plates and stored at 20°C.

Example 9

Quantitation of Hull29

Quantitation of the Hull29 IgG1 antibody secreted into the medium by the COS1 cells was performed using a
 20 sandwich type ELISA. In brief, Nunc Maxisorp Immunoplates* (Nunc#439454) were coated with 50 ul/well of 0.5 ug/ml goat antihuman IgG Fc (Cappel #55071) in 0.1 M sodium bicarbonate pH 9.6 for 3 hours at room temperature. The wells were washed
 25 three times with 0.01 M sodium phosphate pH 7.4, 0.15 M NaCl, 0.1 % Tween*20 (PBS-T). Nonspecific protein binding to the plate was blocked by treatment of the wells with 200 ul/well of 3% (w/v) nonfat dry milk in PBS for 30 minutes at room temperature. A purified human IgG1 kappa standard (Sigma #1-

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3889) was made up at 100 ng/ml in PBS-T and serially diluted 1:2 to 1.56 ng/ml, and 50 ul of each were added to duplicate wells of the assay plate. COS1 cell supernatants were diluted in PBS-T and duplicate 50 ul samples were added to

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the plate. After an one hour room temperature incubation the wells were evacuated and washed three times with PBS-T. To detect the presence of bound Hull 129 antibody, horseradish peroxidase conjugated affinity purified goat anti-human IgG (whole molecule, Cappel #3601-0081) was diluted 1:1 000 in PBS-T and 50 ul was added to each well of the assay plate and incubated at room temperature for one hour. The plate was washed three times with PBS-T and 100 ul of the chromogenic substrate TMB^{blue}* (TSI #TM102) was added to each well. The plate was incubated at room temperature in the dark for ten minutes and the reaction was stopped by the addition of 50 ul per well of 4.5 M H₂SO₄. The plate was read at 450 nm using a Molecular Devices Vmax microplate reader, and data analysis was performed using Softmax software (Molecular Devices) running on an IBM P/S2 model 80 computer.

During the first seventy two hours of production the COS1 cells produced 0.06ug/ml Hull129, for a total of 0.9ug. The next ninety six hours of production the COS1 cells produced 0.99ug/ml Hull129, for a total of 14.85ug.

20 Example 10

Hull129 Binding Assay

Binding assays of the Hull129 were performed in a capture ELISA, essentially as for the quantitation ELISA, but with the following changes. Plates were coated with the Mul 331 antibody at 0.5ug/well, the wells were blocked with 3% non-fat milk in PBS-T, and 50ul of RSV infected HEP2 cell lysate was added to each well and incubated at room temperature for 1 hour. The remainder of the assay was carried out as for the

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quantitation essay starting with the addition of diluted samples to the wells. Results were analyzed as a double reciprocal plot of OD vs antibody concentration from which an

apparent K_d for the H1129 molecule of 0.7nM was determined compared to 10nM for the H1129HuGammal,Kappa antibody.

RSV neutralization assays on H1129 and ch1129 antibody were performed according to the following procedure:

1. Unwrap 96 well Costar cell culture plates in hood.
2. Warm Growth Medium (GM) to 37 C.
3. Thaw MA104 cells at 37 C. Dilute to ~150,000 cells per mL with GM. Mix cells and dispense 200 μ l per well.
4. Culture cells 37 C, 5% CO₂, and humidified overnight before infection.
5. Dilute RSV Stock to 10,000 pfu per mL in Maintenance Medium (MM).
6. Mix equal volume of Antibody diluted in MM with equal volume of diluted RSV. Incubate at 37 C, 5% CO₂, and humidified for 1.0 h before infection.
7. Infect replicate wells of MA104 cells with 200 μ l of the Antibody and Virus mixture. Infect replicate wells with virus and mock infected controls.
8. Wrap the plates in cellophane and incubate at 37 C, 95% humidity, and 5% CO₂ for 5 days.
9. ELISA for RSV. Aspirate each well; add 100 μ l 80% Acetone/PBS (vol./vol.) and incubate at room temperature 30 minutes.

10. Aspirate each well and air dry for 30 minutes on the grill of a laminar flow hood.
11. Wash 4 times with PBS, 0.05% Tween 20.
12. Add 100 μ l of monoclonal antibody to RSV F-protein to each well. Incubate for 1.0 h at 37 C.
13. Wash 4 times with PBS, 0.05% Tween 20.
14. Add 100 μ l of anti-murine antibody goat serum-horse radish peroxidase conjugate to each well. Incubate for 1.0 h at 37 C.
15. Wash 4 times with PBS, 0.05% Tween 20.
16. Add 100 μ l of a freshly prepared 1:1 mixture of ABTS and peroxide to each well. Incubate at room temperature until the optical density (405 nm) of the virus control is 5 to 10 times that of the mock infected controls.

Appendix:

Growth Medium (GM): Minimum Essential Medium (Eagle) with Earle's BSS,
2mM glutamine,
Eagle's non-essential amino acids 0.1 mM final,
Fetal bovine serum 10% (v/v),
Penicillin 50 units/ml,
Streptomycin 50 mcg/ml

Maintenance Medium (MM): as above with serum reduced to 1 to 2%.

MA104 cell stocks are grown up in T150 flasks with Growth Medium. Stocks are frozen at 3×10^6 cells per 1.8 mL vial in 10% DMSO and Growth Medium. Stored in a LN₂ refrigerator.

RSV stocks: are grown up in MA104 (monkey kidney) or Hep 2 cells in T150 flasks. Add ~0.2mL (~100,000 pfu) virus stock per confluent T150. Adsorption for 1.0 h at room temperature. Then add 20 mL maintenance medium with 1% fetal bovine serum. Incubate 4-5 days at 37°C. Collect cells just before 100% cpe by scraping. Spin down cells; remove all but 10 mL of supernatant. Freeze (dry ice-ethanol bath) thaw cell pellet, vortex, re-freeze, and store virus stock in LN₂ refrigerator.

ELISA Antibody Buffer: PBS, 0.05% Tween 20 (w/v), 2.0% goat serum (v/v) and 0.5% gelatin (w/v).

RSV F Protein Antibody: Chemicon Mab 858-1 anti-RSV fusion protein diluted ~1: 5000 in ELISA Antibody Buffer.

Anti-Murine Serum: Fisher horse radish peroxidase conjugated to goat anti-mouse IgG (Heavy Chain Specific) diluted ~1: 4000 in ELISA Antibody Buffer.

The results are shown in Figure 10, and indicate 25ng/mL achieved 50% neutralization in this assay while 45ug/mL of the H1129 antibody was required for 50% neutralization in this experiment. Over a series of 6 separate assays the mean 50% neutralization value for H1129 was 17ng/mL. As a control and to compare potency we also assayed a polyclonal human IgG preparation made from the plasma of individuals with high neutralizing titers for RSV. This preparation, termed RSVig

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(lot#4), gave a mean 50% neutralization value of 2.3ug/ml over 3 experiments. Thus the H1129 is 100-fold more potent in this assay as the enriched polyclonal preparation.

Example 11

5 Kinetic Analysis of Humanized RSV Mabs by BIAcore™

The kinetics of interaction between humanized RSV Mabs and the RSV F protein was studied by surface plasmon resonance using a Pharmacia BIAcore™ biosensor. A recombinant baculovirus expressing a C-terminal truncated F protein provided an
10 abundant source of antigen for kinetic studies. The supernatant, which contained the secreted F protein, was enriched approximately 20-fold by successive chromatography on concanavalin A and Q-sepharose* columns. The pooled fractions were dialyzed against 10 mM sodium citrate (pH 5.5), and
15 concentrated to approximately 0.1 mg/ml. An aliquot of the F-protein (100 ml) was amine-coupled to the BIAcore sensor chip. The amount immobilized gave approximately 2000 response units (Rmax) of signal when saturated with either H1129 or H1308F. This indicated that there was an equal number of "A" and "C"
20 antigenic sites on the F-protein preparation following the coupling procedure. Two unrelated irrelevant Mabs (RVFV 4D4 and CMV H758) showed no interaction with the immobilized F protein. A typical kinetic study involved the injection of 35 ml of Mab at varying concentrations (25-300 nM) in PBS buffer
25 containing 0.05% Tween-20 (PBS/Tween). The flow rate was maintained at 5 ml/min, giving a 7 min binding phase. Following the injection of Mab, the flow was exchanged with PBS/Tween buffer for 30 min for determining the rate of dissociation. The sensor chip was regenerated between cycles
30 with a 2 min pulse of 10 mM HCl.

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The regeneration step caused a minimal loss of binding capacity of the immobilized F-protein (4% loss per cycle). This small decrease did not change the

calculated values of the rate constants for binding and dissociation.

The affinity of the various Mabs for binding to the F protein was calculated from the ratio of the first order rate constant for dissociation to the second order rate constant for binding ($K_d = k_{diss}/k_{assoc}$). The value for k_{assoc} was calculated based on the following rate equation:

$$(1) \quad dR/dt = k_{assoc}[Mab]R_{max} - (k_{diss}[Mab] + k_{diss})R$$

where R and Rmax are the response units at time t and infinity, respectively. A plot of dr/dt as a function of R gives a slope of $(k_{assoc}[Mab] + k_{diss})$. Since these slopes are linearly related to the [Mab], the value k_{assoc} can be derived from a replot of the slopes versus [Mab]. The slope of the new line is equal to k_{assoc} . Although the value of k_{diss} can be extrapolated from the Y-intercept, a more accurate value was determined by direct measurement of k_{diss} . Following the injection phase of the Mab, PBS/Tween buffer flows across the sensor chip. From this point, [Mab] = 0. Equation (1) thus reduces to:

$$(2) \quad dr/dt = -k_{diss}R \quad \text{or} \quad dR/R = -k_{diss}dt$$

Integration of equation (2) gives:

$$(3) \quad \ln(R_0/R_t) = k_{diss}t$$

where R_0/R_t are the response units at time 0 (start of dissociation phase) and t, respectively. Lastly, plotting $\ln(R_0/R_t)$ as a function of t gives a slope of k_{diss} .

Kinetic Constants for RSV Mab

(K _a /K _d)	K _a (assoc)	K _d (dissoc)	t _{1/2} #	K	d
Mab	M ⁻¹ sec ⁻¹	sec ⁻¹	(Hrs)		nM
CH1129	5.0 X 10 ⁴	7.5 X 10 ⁻⁵	2.6		1.5
H1129	4.9 X 10 ⁴	6.9 X 10 ⁻⁵	2.8		1.4
M1129	3.5 X 10 ⁴	4.0 X 10 ⁻⁴	0.48		11.4
M1308F	3.5 X 10 ⁴	3.8 X 10 ⁻⁵	5.1		1.1
H1308F	2.2 X 10 ⁴	5.5 X 10 ⁻⁵	3.5		2.5

Example 12

In vivo Protection of Cotton Rats with Humanized Mab's
 H1129 and H1308F were each tested for the ability to reduce infection in the lung tissue of cotton rats when administered intra-muscularly. Cotton rats (*S. hispidus*, 4 animals per group, average weight 100 grams) were anesthetized with methoxyflurane and given 0.1 ml of antibody solution, resulting in doses of 5mg/kg, 1.67mg/kg and 0.56 mg/kg respectively) by intra-muscular injection. Control animals were injected with bovine serum albumin. One day later, animals were again anesthetized and challenged by intra-nasal instillation of 10^{4.0} plaque forming units (PFU) of the Long strain of RSV. Four days after virus challenge, all animals were sacrificed by carbon dioxide asphyxiation. Lungs were harvested and homogenized in 10 parts (wt/vol) Hanks balanced salt. The resulting suspension was quantified for virus content by plaque assay.

The results of these experiments, shown below, indicate that both H1129 and H1308F are effective in reducing

viral titers in the lungs of cotton rats when injected one day before RSV challenge.

<u>Antibody</u>	<u>Injected Dose</u>	<u>Virus Titer (pfu/cm)</u> <u>in Lung Tissue</u>
None		6.3×10^4
Humanized 1129	5 mg/kg	1.2×10^2
	1.67 mg/kg	1.4×10^2
	0.56 mg/kg	5.7×10^3
Murine 1308F	5 mg/kg	6.8×10^3
	1.67 mg/kg	1.3×10^4
	0.56 mg/kg	2.6×10^4
Humanized 1308F	5 mg/kg	2.7×10^3
	1.67 mg/kg	1.3×10^4
	0.56 mg/kg	2.1×10^4

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: MEDIMMUNE, INC.

(ii) TITLE OF INVENTION: HUMAN-MURINE CHIMERIC ANTIBODIES AGAINST
RESPIRATORY SYNCYTIAL VIRUS

(iii) NUMBER OF SEQUENCES: 49

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SMART & BIGGAR

(B) STREET: P.O. BOX 2999, STATION D

(C) CITY: OTTAWA

(D) STATE: ONT

(E) COUNTRY: CANADA

(F) ZIP: K1P 5Y6

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: ASCII (text)

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: SMART & BIGGAR

(B) REGISTRATION NUMBER:

(C) REFERENCE/DOCKET NUMBER: 68975-178

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (613)-232-2486

(B) TELEFAX: (613)-232-8440

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 27 BASE PAIRS

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCGGATCCA GGGGCCAGTG GATAGAC

27

10 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 17 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGGATGGTGG GAAGATG

17

20 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 15 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCCAGTGA TAGAC

15

30 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 16 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TACAGTTGGT GCAGCA

16

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 24 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATGGATCCA GTTGGTGCAG CATC

24

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 30 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CACGTCGACA TTCAGCTGAC CCAGTCTCCA

30

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 30 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGGAATTCAG GTNNANCTGC AGNAGTCWGG

30

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 28 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCCAAGCTTG GTCCCCCTC CGAACGTG

28

10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 39 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGCGTCGACT CACCATGGAC ATGAGGGTCC YGCTCAGC

39

20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 57 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTCACCATCA CTTGCAAGTG CCAGCTGACT GTAGGTTACA TGCACTGGTA CCAGCAG

57

30

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 54 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCAACTTATT ACTGCTTTCA GGGGAGTGGG TACCCATTCA CGTTCGGAGG GGGG

54

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 32 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTGACCAACA TGGACCTGCG TGATACTGCC AC

32

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 29 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCATGTTGGT CACTTTAAGG ACCACCTGG

29

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 37 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCAGTTTACT AGTGTTCATAG ATCAGGAGCT TAGGGGC

37

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 37 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGACACTAGT AAACCTGGCTT CTGGGGTCCC ATCAAGG

37

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 97 AMINO ACIDS

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

20 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
 1 5 10 15
 Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn
 20 25 30
 Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 35 40 45
 30 Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr
 50 55 60
 Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
 65 70 75
 Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
 80 85 90
 Thr Ala Val Tyr Tyr Cys Ala
 95

40

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 117 AMINO ACIDS

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

10 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
 1 5 10 15
 Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys
 20 25 30
 Asp Tyr Tyr Ile Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 35 40 45
 Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Val Phe
 50 55 60
 Asp Pro Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
 65 70 75
 20 Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
 80 85 90
 Thr Ala Val Tyr Tyr Cys Ala Tyr Tyr Gly Thr Ser Ser Phe Asp
 95 100 105
 Phe Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
 110 115

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 117 AMINO ACIDS

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

40 Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 1 5 10 15
 Ala Leu Val Lys Leu Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys
 20 25 30
 Asp Tyr Tyr Ile Tyr Trp Val Lys Gln Arg Pro Glu Gln Gly Leu
 35 40 45
 Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Val Phe
 50 55 60
 50 Asp Pro Lys Phe Gln Gly Lys Ala Ser Ile Thr Ser Asp Thr Ser
 65 70 75
 Ser Asn Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp
 80 85 90
 Thr Ala Val Tyr Tyr Cys Ala Tyr Tyr Gly Thr Ser Ser Phe Asp

	95	100	105
Phe Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser			
	110	115	

(2) INFORMATION FOR SEQ ID NO:19

(i) SEQUENCE CHARACTERISTICS

- 10 (A) LENGTH: 95 AMINO ACIDS
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val	
1 5 10 15	
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser	
20 25 30	
Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
35 40 45	
Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser	
50 55 60	
Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile	
65 70 75	
30 Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln	
80 85 90	
Tyr Asn Ser Tyr Ser	
95	

(2) INFORMATION FOR SEQ ID NO:20

(i) SEQUENCE CHARACTERISTICS

- 40 (A) LENGTH: 107 AMINO ACIDS
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val	
1 5 10 15	
Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn	
20 25 30	
Arg Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
35 40 45	

Leu Leu Ile Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser
 50 55 60
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
 65 70 75
 Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
 80 85 90
 10 Phe His Glu Phe Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu
 95 100 105
 Ile Lys

(2) INFORMATION FOR SEQ ID NO:21

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 107 AMINO ACIDS

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Met Tyr Val Ser Leu
 1 5 10 15
 Gly Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn
 20 25 30
 30 Arg Tyr Leu Asn Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys
 35 40 45
 Thr Leu Ile His Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser
 50 55 60
 Arg Phe Ser Gly Ser Gly Ser Gly Gln Glu Tyr Ser Leu Thr Ile
 65 70 75
 40 Ser Ser Leu Glu Phe Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln
 80 85 90
 Phe His Glu Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
 95 100 105
 Ile Lys

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 117 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCATGGACTG GACCTGGAGG GTCCTCTGCT TGCTGGCTGT AGCACCAGGT GCCCACTCCC 60
AGGTGCAGCT GGTGCAGTCT GAGCTGAGG TGAAGAAGCC TGGAGCCTCA GTGAAGG 117

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 120 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CACTTCTTCG GACCTCGGAG TCACTTCCAA AGGACGTCC GTAGACCTAA GTTGTAATTC 60
CTGATGATGT AAATGACCCA CGCTGTCCGA GGACCTGTC CCGAGCTCAC CTACCCAACC 120

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 119 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGGCTCGAGT GGATGGGTTG GATTGACCCT GAGAATGATA ATACTGTGTT TGACCGAAGT 60
TCCAGGGCAG AGTCACCATG ACCAGGGACA CGTCCACGAG CACAGTCTAC ATGGAGCTG 119

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 137 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGTGCTCGTG TCAGATGTAC CTCGACTCGT CGGACTCTAG ACTCCTGTGC CGGCACATAA 60
 TGACACGCAT GATGCCATGT TCGAGGAAAC TGAAGACCCC GGTCCCGTGG TGAGAGTGTG 120
 ACTCGAGTAT TCCTAGG 137

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 106 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCATGGAGAT GAGGGTCCCC GTCAGCTCC TGGGGCTCCT GCTGCTCTGG CTCCCAGGTG 60
 CCAAAATGTA TATCCAGATG ACCCAGTCTC CTTCACCCCT GTCTGC 106

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 107 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTCAGAGGAA GGTGGGACAG ACGTAGACAT CCTCTGTCTC AGTGGTAGTG AACGTTCGGC 60
 TCAGTCTCTG TAATTATCCAT AAATTGACC ATGGTCGTCT TTGGGCC 107

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 107 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAAAGCCCCCT AAGCTCCTGA TCTATCGTGC AAACAGATTG GTAGATGGGG TCCCATCAAG 60
 GTTCAGCGGC AGTGGATCTG GACAGAAIT CACTCTCACC ATCAGCA 107

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 116 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTCTTAAGTG AGAGTGGTAG TCGTCGGACG TCGGACTACT AAAACGTTGA ATAATGACGG 60
 ATGTCAAAGT ACTCAAAGGC AAGTGCAAGC CTCCCCCTG GTTCGAACIT TATTTT 116

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 123 AMINO ACIDS

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Gln	Val	Thr	Leu	Arg	Glu	Ser	Gly	Pro	Ala	Leu	Val	Lys	Pro	Thr	1	5	10	15
Gln	Thr	Leu	Thr	Leu	Thr	Cys	Thr	Phe	Ser	Gly	Phe	Ser	Leu	Ser	20	25	30	
Ser	Ser	Gly	Met	Cys	Val	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	35	40	45	
Ala	Leu	Glu	Trp	Leu	Ala	Asp	Ile	Glu	Trp	Asp	Asp	Asp	Lys	Asp	50	55	60	
Tyr	Asn	Thr	Ser	Leu	Asp	Thr	Arg	Leu	Thr	Ile	Ser	Lys	Asp	Thr	65	70	75	
Ser	Lys	Asn	Gln	Val	Val	Leu	Thr	Val	Thr	Asn	Met	Asp	Pro	Ala	80	85	90	
Asp	Thr	Ala	Thr	Tyr	Tyr	Cys	Ala	Arg	Ile	Thr	Val	Ile	Pro	Ala	95	100	105	
Pro	Ala	Gly	Tyr	Met	Asp	Val	Trp	Gly	Arg	Gly	Thr	Pro	Val	Thr	110	115	120	

Val Ser Ser

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 120 AMINO ACIDS

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

10 (ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr
 1 5 10 15
 Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser
 20 25 30
 Thr Ser Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys
 35 40 45
 20 Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp
 50 55 60
 Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr
 65 70 75
 Ser Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala
 80 85 90
 30 Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp
 95 100 105
 Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 110 115 120

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 120 AMINO ACIDS

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

40 (ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gln Val Glu Leu Gln Glu Ser Gly Pro Gly Ile Leu Gln Pro Ser
 1 5 10 15
 Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser
 20 25 30
 50 Thr Ser Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Glu
 35 40 45

Gly Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp
 50 55 60
 Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr
 65 70 75
 Ser Ser Asn Gln Val Phe Leu Lys Ile Thr Gly Val Asp Thr Ala
 80 85 90
 10 Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp
 95 100 105
 Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 110 115 120

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS

- 20 (A) LENGTH: 95 AMINO ACIDS
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
 1 5 10 15
 Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
 20 25 30
 30 Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 35 40 45
 Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser
 50 55 60
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
 65 70 75
 40 Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 80 85 90
 Tyr Asn Ser Tyr Ser
 95

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS

- 50 (A) LENGTH: 106 AMINO ACIDS
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:


```

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
 1          5          10          15
Gly Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly
          20          25          30
Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
          35          40          45
10 Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg
          50          55          60
Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
          65          70          75
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly
          80          85          90
20 Ser Gly Tyr Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
          95          100          105
Lys

```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 106 AMINO ACIDS

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

30 (ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro
 1          5          10          15
Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Gly
          20          25          30
Tyr Met His Trp Tyr Gln Gln Lys Ser Ser Thr Ser Pro Lys Leu
          35          40          45
40 Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Gly Arg
          50          55          60
Phe Ser Gly Ser Gly Ser Gly Asn Ser Tyr Ser Leu Thr Ile Ser
          65          70          75
Ser Ile Gln Ala Glu Asp Val Ala Thr Tyr Tyr Cys Phe Gln Gly
          80          85          90
50 Ser Gly Tyr Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
          95          100          105
Lys

```

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 63 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCCTGAGCTC ACGGTGACCG TGSTCCCGCC GCCCCAGACA TCGAGTAGC AGTTCGTGAT CAT 63

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 79 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTGTGTGACT ITAAGGACCA CTTGGTTTTT GGAGGTATCC TTGGAGATTG TGAGCCGGCT 60
 CTTGAGCCAT GGATTATAG 79

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 89 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GCGCCTCCCC TGGGGGCTGA CGAATCCAGC CTACACTCAT ACCAGAAGTG CTCAGTGAAA 60
 ACCCAGAGAA GGTGGAGGTC AGTGTGAGG 89

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 70 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCAGGTCACC TTAAGGGAGT CTGGTCCTGC GCTGGTGAAA CCCACACAGA CCCTCACACT 60
GACCTGCACC 70

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 78 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CAGCCCCCAG GGAAGGCCCT GGAGTCGCTT GCAGACATTT GGTGGGATGA CAAAAGGAC 60
TATAATCCAT CCCTGAAG 78

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 64 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGTCCTTAAA GTGACCAACA TGGACCTGCG TGATACIGCC ACTTACTACT GTGCTCGGTC 60
TATG 64

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 72 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGCGTCGACT CACCATTGGAC TGGACCTGGA GGGCTCTTCTG CTTGCTGGCT GTAGCACCAG 60
GTGCCCCACTC CC 72

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 7 AMINO ACIDS

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Thr Ser Gly Met Ser Val Gly
1 5

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 16 AMINO ACIDS

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 10 AMINO ACIDS

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ser Met Ile Thr Asn Trp Tyr Phe Asp Val
1 5 10

- (2) INFORMATION FOR SEQ ID NO:46:
- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 10 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Lys Cys Gln Leu Ser Val Gly Tyr Met His
 5 10

10

- (2) INFORMATION FOR SEQ ID NO:47:
- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 6 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

20 Thr Ser Lys Leu Ala Ser
 1 5

- (2) INFORMATION FOR SEQ ID NO:48:
- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 8 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
 - (ii) MOLECULE TYPE: PROTEIN
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

30

Phe Gln Gly Ser Gly Tyr Pro Phe
 1 5

- (2) INFORMATION FOR SEQ ID NO:49:
- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 6 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR

40

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ser Val Gly Tyr Met His
 1 5

10

68975-178(s)

CLAIMS:

1. A neutralizing antibody against respiratory syncytial virus (RSV), comprising:

5 a human constant region and a variable region, said variable region comprising heavy and light chain framework regions and heavy and light chain complementarity determining regions (CDRs) at least a portion of the heavy and light chain framework regions being derived from a human antibody, said neutralizing antibody against RSV binding to the same epitope
10 as an antibody comprising three heavy chain CDRs comprising amino acids 31-37, 52-67 and 100-109 of SEQ ID NO: 31, and three light-chain CDRs comprising amino acids 24-33, 51-56 and 89-96 of SEQ ID NO: 34.

2. The neutralizing antibody of claim 1 wherein the
15 heavy chain framework comprises the heavy chain framework of SEQ ID NO: 31.

3. The neutralizing antibody of claim 1 wherein the light chain framework comprises the light chain framework of SEQ ID NO: 34.

20 4. The neutralizing antibody of claim 1 wherein the light chain framework comprises the light chain framework of SEQ ID NO: 34 and the heavy chain framework comprises the heavy chain framework of SEQ ID NO: 31.

5. The neutralizing antibody of claim 1 wherein the
25 heavy chain of the neutralizing antibody comprises the polypeptide of SEQ ID NO: 31.

6. The neutralizing antibody of claim 1 wherein the light chain of the neutralizing antibody comprises the polypeptide of SEQ ID NO: 34.

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7. The neutralizing antibody of claim 1 wherein the heavy chain of the neutralizing antibody comprises SEQ ID NO: 31 and the light chain of the antibody comprises SEQ ID NO: 34.

8. A neutralizing antibody against respiratory syncytial virus, comprising:

a human constant region and a heavy and light chain variable region, said heavy and light chain variable region comprising heavy and light chain framework regions and heavy and light chain CDRs at least a portion of the heavy and light chain framework regions being derived from a human antibody, said CDRs comprising three heavy-chain CDRs comprising amino acids 31-37, 52-67 and 100-109 of SEQ ID NO: 31 and three light-chain CDRs comprising amino acids 24-33, 51-56 and 89-96 of SEQ ID NO: 34.

9. A pharmaceutical composition comprising:

- (a) the neutralizing antibody of claim 1 and
- (b) a pharmaceutically acceptable diluent.

10. A pharmaceutical composition comprising:

- (a) the neutralizing antibody of claim 2 and
- (b) a pharmaceutically acceptable diluent.

11. A pharmaceutical composition comprising:

- (a) the neutralizing antibody of claim 3 and
- (b) a pharmaceutically acceptable diluent.

12. A pharmaceutical composition comprising:

- (a) the neutralizing antibody of claim 4 and
- (b) a pharmaceutically acceptable diluent.

13. A pharmaceutical composition comprising:

- (a) the neutralizing antibody of claim 5 and
- (b) a pharmaceutically acceptable diluent.

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14. A pharmaceutical composition comprising:
- (a) the neutralizing antibody of claim 6 and
 - (b) a pharmaceutically acceptable diluent.
15. A pharmaceutical composition comprising:
- 5 (a) the neutralizing antibody of claim 7 and
 - (b) a pharmaceutically acceptable diluent.
16. A pharmaceutical composition comprising:
- (a) the neutralizing antibody of claim 8 and
 - (b) a pharmaceutically acceptable diluent.
- 10 17. The neutralizing antibody of claim 8 wherein the heavy chain framework comprises the heavy chain framework of SEQ ID NO: 31.
18. The neutralizing antibody of claim 8 wherein the light chain framework comprises the light chain framework of
- 15 SEQ ID NO: 34.
19. A use of the neutralizing antibody according to any one of claims 1 to 8, 17 and 18 for the protection of a human from respiratory syncytial virus infection.
20. A pharmaceutical composition comprising:
- 20 (a) the neutralizing antibody of claim 17 and
 - (b) a pharmaceutically acceptable diluent.
21. A pharmaceutical composition comprising:
- (a) the neutralizing antibody of claim 18 and
 - (b) a pharmaceutically acceptable diluent.

FIG. 1A

5 10 15 20
 Gln Val Gln Leu Val Gln Ser Gly Ala Gln Val Lys Lys Pro Gly Ala Ser Val Lys Val Harn H₂O Val
 *
 Gln Val Gln Leu Val Gln Ser Gly Ala Gln Val Lys Lys Pro Gly Ala Ser Val Lys Val *CTR Grafted* Val
 *
 Gln Val Gln Leu Val Gln Ser Gly Ala Gln Leu Val Asp Pro Gly Ala Leu Val Lys Leu Marine 1308F Val

25 30 35 40
 Ser Qys Lys Ala Ser Gly Tyr Thr Phe Asn Ser Tyr Tyr Met His Trp Val Asp Gln Ala
 * * * * *
 Ser Qys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr Tyr Ile Tyr Trp Val Asp Gln Ala
 * * * * * CTR 1
 Ser Qys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr Tyr Ile Tyr Trp Val Lys Gln Arg
 * * * * *
 45 50 55 60
 Pro Gly Gln Gly Leu Gln Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr
 * * * * *
 Pro Gly Gln Gly Leu Gln Asp Ile Gly Tyr Ile Asp Pro Gln Asn Gly Asn Thr Val Phe
 * * * * * CTR 2
 Pro Gln Gln Gly Leu Gln Trp Ile Gly Tyr Ile Asp Pro Gln Asn Gly Asn Thr Val Phe
 * * * * *

65 70 75
 Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Thr Val Tyr
 * * * * *
 Asp Pro Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Thr Val Tyr
 * * * * *
 Asp Pro Lys Phe Gln Gly Lys Ala Ser Ile Thr Ser Asp Thr Ser Ser Asn Thr Ala Tyr
 * * * * *

MATCH WITH FIG. 1B

MATCH WITH FIG. 1A

FIG. 1B

80/81 82a 82b 82c 83 90 95
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Tyr Tyr Gly
 *
 Leu Glu Leu Ser Ser Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Tyr Tyr Gly
 105 110
 Thr Ser Ser Phe Asn Phe Trp Gly Glu Gly Thr Thr Leu Thr Val Ser Ser
CIR 3
 Thr Ser Ser Phe Asp Phe Trp Gly Glu Gly Thr Thr Leu Thr Val Ser Ser
 J>>

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FIG. 2A

	5	10	15	20
Asp Ile Gln Met Thr Gln Ser Pro Ser	Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr	- Human R102 VL		
Asp Ile Gln Met Thr Gln Ser Pro Ser	Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr	- "CCR Grafted" VL		
Asp Ile Lys Met Thr Gln Ser Pro Ser	Met Tyr Val Ser Leu Gly Gln Arg Val Thr	- Murine 1300P VL		
	25	30	35	40
Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser	Trp Leu Ala Trp Tyr Gln Gln Lys Pro			
Ile Thr Cys Met Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro				
Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Arg Tyr Leu Asn Trp Phe Gln Gln Lys Pro				
	45	50	55	60
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Ser				
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asn Ala Asn Asn Leu Val Asn Gly Val Pro Ser				
Gly Lys Ser Pro Lys Thr Leu Ile His Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser				

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MATCH WITH FIG. 2B

MATCH WITH FIG. 2A

105 - - - - -
Gly Thr Lys Leu Glu Ile Lys
Gly Thr Lys Leu Glu Ile Lys

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MATCH WIT FIG. 3B

MATCH WITH FIG. 3A

ProLysPheGlnGlyArgValThrMetThrArgAspThrSerThrSerThrValIleYrMet
CCTAAGTTCACGGCCAGAGTCACCATTGCCAGTGTCACGTCCACAGCATCGTTCAATG
241 +-----+
GGCTCAAGGTCCCGTCTTCAAGTGGTACTGTGTGCCTGTGCAAGTSCCTGGTCAGAGAGAAC

GluLeuSerGlnArgSerGluAspThrAlaValTyrTyrCysAlaIleTyrTyGlyThr
GGCTGTACCAAGCCCTCGATCATCTGGAGCACGCCGCCTGTATTACTTGTCGTACTACGTTACA

301

Ser.Ser.Phe.Asp.Phe.Trp.Ile.Gly.Ind.Leu.Lys.Val.Ser.Ser
AGCTTCCTTCACTTCGTGGGCGCAGGCCACCACTCATCACATGAGCTCA
36)-----+-----+-----+-----+-----+-----
TCGGGGAACCTGAGAGACCCCGGTTCCGGTGTAAGTGTACTCTGAGTATTCTAAG 5'
ggcgagcgtcactcgcagtattctcaggcc

Met Asp Met Arg Val Pro AlaGlnLeuLeuGlyIleuLeuLeuTrpLeuProGlyAla
+
gagcctgcggacatcgagggtcccccactgaccttccttggaattccttgcctggccccaggatgcc
)
TACCTTCATCCCAAGGGTGA CTGTGAGGACC CGC AGCACCG GACGACTGC CAA GG

LysCysAspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArg
AAATGGAGTTCGACGAGAACAAGACTCTCGACCCTGTCTCATCTCTAGCAACACGA

TTTACATAATTAGTGCTAC TGG CAGGAGAGTGGGACACAGCCAGAGTCTCTTCTTCT
61

ValThrIleThrCysLysAlaSerGlnAspIleAsnArgTyrLeuAsnTrpTyrGlnGln
GTCACCATCCTCTCCAGCGCAGTCAGACANTATATAGTATTTTAACTGTCGTCACGAC
CAGGCTGAGGAGGCTCCGCTACTCTGTAATTCATCATTAATTCAGCAGGCTGGTC
221

lysProGlyLysAlaProLysLeuLeuIleTyrArgAlaAsnArgLeuValAspGlyVal
AAACCGGGAAACCCCTGACCTGCTGCTATGCTGCAACAGATGGTAGATGGGTC
TTTGGGCGCCTTCGGGGATTCGAGACTAGATAGCACTGTGTCTCAACATCTACCCGAG

MATCH WITH FIG. 4B

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FIG. 4B

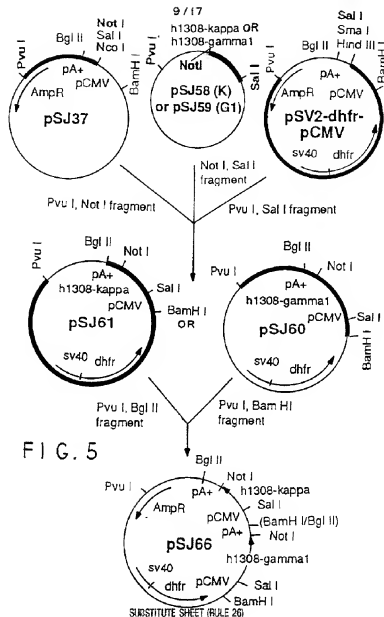
MATCH WITH FIG. 4A

```

ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeu
241  LALLSSAJTCAGGCTGAGTGGATTTGGAGGATATTCCTCTTAAATATGAGAGCCGCG
      +-----+-----+-----+-----+-----+-----+
GGAATTCAGATCGCGCGCTACCTACACCTCTCTTAAAGTGAATATGATGATCTGGAC
      +-----+-----+-----+-----+-----+-----+
GluProAspArgPheAlaThrTyrCysLeuGluPheIleGluPheProCysThrPhe
301  CAGCTGGATGATTTGCACATTATCTACTCTACAGATTCAGATTTCCGTACAGTTC
      +-----+-----+-----+-----+-----+-----+
CTTGAATCTATAAGCTTGAATATGACAGATCTCAAGATGTCATAGCAATGTCAG
      +-----+-----+-----+-----+-----+-----+
GlyGlyGlyThrLysLeuGluIleLys
361  GGAGGGGGACCACTTGAATATAA 3'
      +-----+-----+-----+-----+-----+-----+
CTCTCCCTCCCTGGAGCTTATTT 5'
      +-----+-----+-----+-----+-----+-----+
cctccccctggaggacc 5'
      +-----+-----+-----+-----+-----+-----+
3' ggcgaag

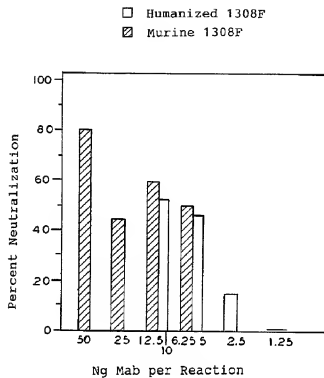
```

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FIG. 6



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FIG. 7A

5
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Human VH (Cor)
 10
 Gln Val Asn Arg Glu Ser Gly Pro Ala Leu Val Lys Ala Thr Human VH (Cass)
 15
 1 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr MED1-493 VH
 Gln Val Glu Leu Glu Glu Ser Gly Ile Leu Gln Pro Ser Murine 1129 VH
 20
 Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser
 His Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Leu Ser Val Asn
 25
 16 Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser
 Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser
 Ser Thr Gly Met Cys Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
 Thr Arg Gly Met Ser Val Ser Trp Ile Arg Gln Pro Pro Gly Lys
 31 Thr Ser Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
 Thr Ser Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Glu
 Gly Leu Glu Trp Leu Ala Arg Ile Glu Trp Asp Asp Lys Tyr
 46 Ala Leu Glu Trp Leu Ala Arg Ile Glu Trp Asp Asp Lys Tyr
 Gly Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Asp
 COR2

MATCH WITH FIG. 7B

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MATCH WITH FIG. 7A

FIG. 7B

Tyr Asn Thr Ser Leu Asp Thr Arg Leu Thr Ile Ser Lys Asp Thr
 Tyr Asn Thr Ser Leu Asp Thr Arg Leu Thr Ile Ser Lys Asp Thr
 61 ~~Tyr Asn Thr Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr~~

Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr

Ser Lys Asn Gln Val Val - - Thr Thr Met Asp Pro Tyr
 Ser Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala
 76 Ser Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala
 * * * * *
 Ser Ser Asn Gln Val Phe Leu Lys Ile Thr Gly Val Asp Thr Ala

Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ile Thr Val Ile Pro Ala Pro Ala Gly
 Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Met Gln Val Thr Met Val Arg Val Met Ile Thr Ser Asn Ala
 91 Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp

CDR3

Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp

Tyr Met Asp Val Trp Gly Arg Gly Thr Pro Val Thr Val Ser Ser
 Ala Phe Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 106 ~~Tyr Phe Asp Val Trp Gly Ala Gly Thr Ile Thr Val Ser Ser~~

Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser

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FIG. 8A

Human K102 VL (germline)
 MEDI-493 VL
 Murine 1129 VL

5 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val 15
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
 Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro
 20 Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser 30
 Gly Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly
 Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Val Gly
 35 Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 45
 Tyr Met His - Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 Tyr Met His - Trp Tyr Gln Gln Lys Ser Ser Thr Ser Pro Lys
 50 Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser 60
 Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser
 Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Gly
 COR 1
 COR 2

MATCH WITH FIG. 8B

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FIG. 8B

MATCH WITH FIG. 8A

65	Arg Phe Ser Gly Ser Gly Thr	70	Glu Phe Thr Leu Thr Ile	75	
	Arg Phe Ser Gly Ser Gly Thr		Glu Phe Thr Leu Thr Ile		
	Arg Phe Ser Gly Ser Gly Ser		Asn Ser Tyr Ser Leu Thr Ile		
80	Ser Ser Leu Glu Pro Asp Phe	85	Ala Thr Tyr Tyr Cys Glu Glu	90	
	Ser Ser Leu Glu Pro Asp Phe		Ala Thr Tyr Tyr Cys Phe Glu		
	Ser Ser Ile Glu Ala Glu Asp		Val Ala Thr Tyr Tyr Cys Phe Glu		
95	Tyr Asn Ser Tyr Ser/Leu Thr	100	Phe Gly Gly Thr Lys Leu Glu Ile Lys	105	
	Gly Ser Gly Tyr Pro Phe Thr		Phe Gly Gly Thr Lys Leu Glu Ile Lys		
	<u>Gly Ser Gly Tyr Pro Phe Thr</u>		<u>Gly Thr Lys Leu Glu Ile Lys</u>		
	<u>COE 3</u>				
	Gly Ser Gly Tyr Pro Phe Thr		Gly Gly Thr Lys Leu Glu Ile Lys		

Human J-Kappa 4

<<V / J>>

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FIG. 9A

SJ153	<i>NotI</i> CCAATGGACTGGACCTGGAGGGTCTTCTGCTGGCTGTAGCACCAGGTGCCACTCC-3'	SJ153 5'-GGCGTCGACTCA- SJ150 5'-CCAG MetAspTrpThrTrpArgValPheCysLeuAlaValAlaProGlyAlaIleSerGln -1/1
SJ150	GTCACTTAAGGGAGTCTGGTCTGCGCTGGTGAACCCACAGACCTCACACTGACC 3'-GGAGTGTGACTGG ValIhrLeuArgGluSerGlyProAlaLeuValLysProThrGlnThrIleuThrLeuThr	SJ149 SJ149
SJ150	TGCACC-3' ACGTGGAGAGACCCAAAAGTGACTCGTGAAGACCATCACTCCGACCTTACGATC CysThrPheSerGlyPheSerLeuSerIhrSerGlyMetSerValGlyTrpIleArgGln	SJ151 5'-CAG SJ149 SJ149
SJ151	CCCCAGGGAAGCCCTGGAGTGGCTTGCAGACATTTGGTGGGATGCACAAAAGGACTAT 3'-GATA GGGGGTCCCTTCCGGG-5' SJ149 ProProGlyLysAlaLeuGluTrpLeuAlaAspIleTrpTrpAspAspLysLysAspTyr	SJ148 SJ148

MATCH WITH FIG. 9B

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FIG. 9B

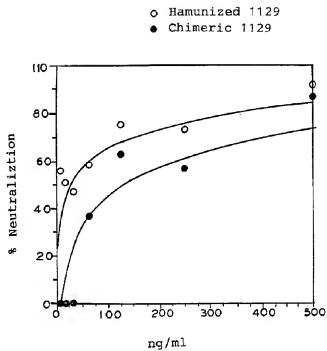
MATCH WITH FIG. 9A

SJ151	AAATCATCCCTGAAG-3' TTAGGTAGGGACTTCTCGGCCGAGGTIAGAGGTTCCTATGGAGTTTGTGTCACAG AsnProSerLeuLysSerArgLeuThrIleSerLysHisValVal	SJ152 5'-GGTC TTAGGTAGGGACTTCTCGGCCGAGGTIAGAGGTTCCTATGGAGTTTGTGTCACAG AsnProSerLeuLysSerArgLeuThrIleSerLysHisValVal	SJ148
SJ152	CTTAAGTGACCAATGAGACCTGCTGATACTGCCACTTACTACTGTGCTGGGTATG GAATTCTACTGGTTC-5' SJ148 LeuLysValThrAsnMetAspProAlaLysThrAlaThrTyrCysAlaArgSerMet	CTTAAGTGACCAATGAGACCTGCTGATACTGCCACTTACTACTGTGCTGGGTATG GAATTCTACTGGTTC-5' SJ148 LeuLysValThrAsnMetAspProAlaLysThrAlaThrTyrCysAlaArgSerMet	SJ147
SJ152	ATCAGCAACTGGTAC-3' TAGTGGCTTGACCATGAAGCTACAGACCCCGCGCCCTGGTCCAGTGGCACTCGAGTCG-5' IleThrAsnTyrPheAspValTrpGlyAlaGlyThrThrValThrValSerSer	ATCAGCAACTGGTAC-3' TAGTGGCTTGACCATGAAGCTACAGACCCCGCGCCCTGGTCCAGTGGCACTCGAGTCG-5' IleThrAsnTyrPheAspValTrpGlyAlaGlyThrThrValThrValSerSer	SJ147

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FIG. 10



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